AMENDMENTS TO THE SPECIFICATION

Kindly replace the paragraph beginning on page 5, at line 7, with the following amended paragraph:

The hypersensitivity regions as identified in the present invention are depicted in Figure 6. One of the preferred hypersensitive regions is the 3'-DHR comprising the nucleic acid sequences from position + 2430 pb to + 3019 bp as shown in Fig. 6. In a more preferred embodiment of the present invention, the 3'DHSR comprises the nucleic acid sequence (SEQ ID NO.:8) GGAAGGTTGAGTCAAGGATT. In an even more preferred embodiment of the present invention, the 3'-DHSR comprises the nucleic acid molecule TGAGTCA. As used herein, the 3-DHSR sequences also comprise sequences containing alterations compared to the particular sequences shown in the figures or to the published sequences which do not lead to a loss of the function as cis-acting element, e.g. as regards gene expression.

Kindly replace the paragraph beginning on page 14, at line 25, and ending on page 15, with the following amended paragraph:

Band-shift analysis of the AP-1 site located within the 1. intron of the MCP-1 gene. A: 2,5 αg "44" extract was incubated with a ^{32}P-labeled oligonucleotide from position +247/+267 (GATAAGGTGACTCAGAAAAGG, (SEQ ID NO.:9) refered as AP-1(I), see schematic presentation depicted below. Lane 1: without competition, lane 2: addition of a 100-fold molar excess of unlabeled homologous oligonucleotides ("homol. comp.(AP-1(I)); lane 3: addition of a 100-fold molar excess of an oligonucleotide haboring a recognition site for the transcription factor NF-1 ("heter. comp."); lane 4: competition with a 100-fold excess of an oligonucleotide containing an AP-1 site of the human collagenase gene ("comp. AP-1 consensus")

B: First four lanes represent band-shift analysis using the AP-1 (I) oligonucleotide (AP-1 (I)) after incubation with nuclear extracts derived from control (-) and TNF-α treated (+) "44"- and "CGL3" cells. Right two lanes represent band-shift pattern of an AP-1 oligonucleotide from the human collagenase gene (AP-1 cons.) using either "44"- or "CGL3" nuclear extracts. Cells were treated with TNF-α (250 U/ml) for 5 h. The position of the AP-1 specific DNA protein complex is indicated. The schematic presentation below shows the location and the sequence of the AP-1 (I) site within the 1st intron relative to the genome organization of the MCP-1 gene.

Kindly replace the paragraph beginning on page 18, at line 2, with the following amended paragraph:

(J) Electrophoretic mobility shift assays

To analyse protein/DNA interactions by electrophoretic mobility shift assays (EMSAs), the following oligonucleotides were used: the AP-1 binding site (SEQ ID NO.:10) (5'GGAAGGTTGAGTCAAGGGATT-3') located within the DNAse I hypersensitive site downstream of the MCP-1 gene (pos. +2587 / +2607), an AP-1 consensus sequence, (SEQ. ID NO.:11) 5'CGCTTGATGACTCAGCCGGAA-3' (Lee et al., Cell 49 (1987), 741-752), an oligonuoleotide containing a recognition site for the nuclear factor 1 (NF-1) derived from the adenovirus origin, 5'-TTTTGGATTGAAGCCAATATGATAA-3' (SEQ ID NO.:12) (Kenny and Hurwitz, J. Bil. Chem. 263 (1988), 9809-9817). The DNAs were synthesized using a phosphoramitide chemistry (Applied Biosystems synthesizer) and further purified by HPLC. Preparation of nuclear extracts, electrophoretic mobility shift and supershift assays were performed exactly as described (Soto et al., Oncogene 18 (1999), 3187-3198).

Kindly replace the paragraph beginning on page 22, at line 1, with the following amended paragraph:

Scanning the 3'-end for potential regulatory sequences, an additional downstream AP-1 site (5'-TGAGTCA-3'; pos. +2594/+2600) (Fig. 6) could be detected. To prove the functionality of this sequence in terms of DNA binding, electrophoretic band-shift assays were performed. Using the oligonucleotide (SEQ ID NO.:10) 5'-GGAAGGTTGAGTCAAGGGATT-3' (pos. +2587/+2607), a single band can be visualized after incubation with a nuclear extract obtained from "444"-cells (Fig. 7A, lane 1). The specificity of AP-1 binding was confirmed in competition experiments by adding a 100-fold molar unlabeled excess of either the homologous oligonucleotide (SEQ ID. NO.:10) (lane 2; "hom. comp. AP-1 3'", 5'-GGAAGGTTGAGTCAAGGGATT-3') or a oligonucleotide containing the AP-1 site (lane 4; "comp. AP-1 consensus", (SEQ ID NO.:11) 5'CGCTTGATGACTCAGCCGGAA-3') of the collagenase TPA responsive element, leading in both cases to complete disappearance of the 3'-AP-1 retarded band. No competition, however, could be achieved, when a heterologous, nuclear factor 1 ("NF-1") specific oligonucleotide (lane 3; "hetero.comp. NF-1", (SEQ ID NO.:12) 5'-TTTTGGATTGAAGCCAATATGATAA-3') was applied. In order to discern whether or nor the extent of AP-1 binding is different between "444"- and "CGL3"-cells and whether the affinity was modulated by TNF-α, the binding properties of different extracts were analysed in the same polyacrylamide gel (Fig. 7B). Although "CGL3"-cells lack MCP-1 expression (see Fig. 1 and 2), all nuclear extracts showed identical binding affinity independently of whether the cells were treated with TNF-α or not prior to cell harvesting (Fig. 7B, lanes 1-4). The absence of enhanced AP-1 binding was not an exceptional feature of the 3'-AP-1 site, because the affinity to the collagenase specific site was also significantly altered (Fig. 7B, lanes 5 and 6).